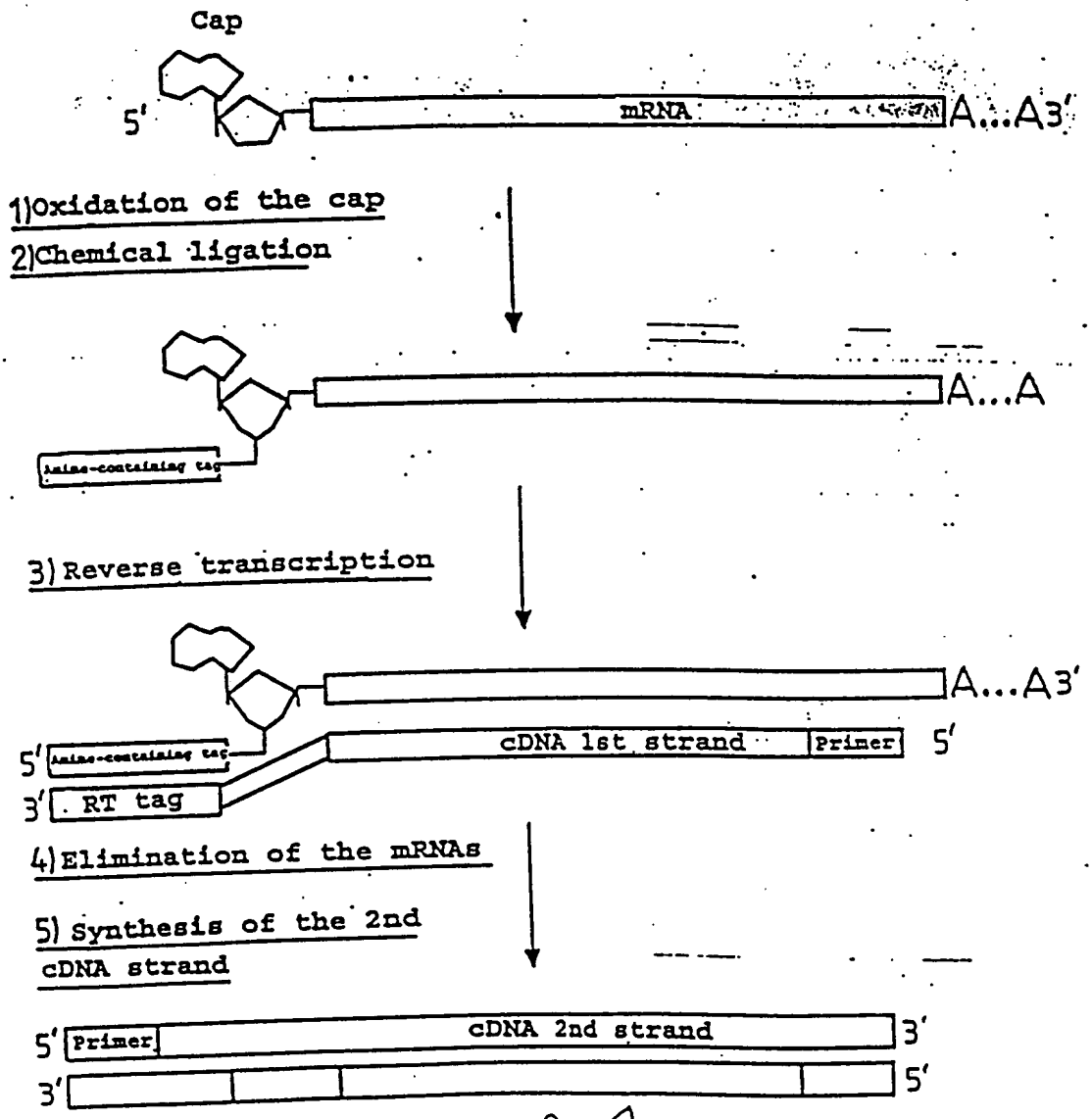

Cap
5'
mRNA
A...A3'
1)Oxidation of the cap
2)Chemical ligation
A...A
Amine-containing tag
3) Reverse transcription
A...A3'
5'
Amine-containing tag
cDNA 1st strand
Primer
5'
3'
RT tag
4) Elimination of the mRNAs
5) Synthesis of the 2nd cDNA strand
5'
Primer
cDNA 2nd strand
3'
3'
5'

FIGURE 1

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3,5	0,121	0,036	0,467	0,664
4	0,096	0,06	0,519	0,708
4,5	0,078	0,079	0,565	0,745
5	0,062	0,098	0,615	0,782
5,5	0,05	0,127	0,659	0,813
6	0,04	0,163	0,694	0,836
6,5	0,033	0,202	0,725	0,855
7	0,025	0,248	0,763	0,878
7,5	0,021	0,304	0,78	0,889
8	0,015	0,368	0,816	0,909
8,5	0,012	0,418	0,836	0,92
9	0,009	0,512	0,856	0,93
9,5	0,007	0,581	0,863	0,934
10	0,006	0,679	0,835	0,918

FIGURE 2

Score curves

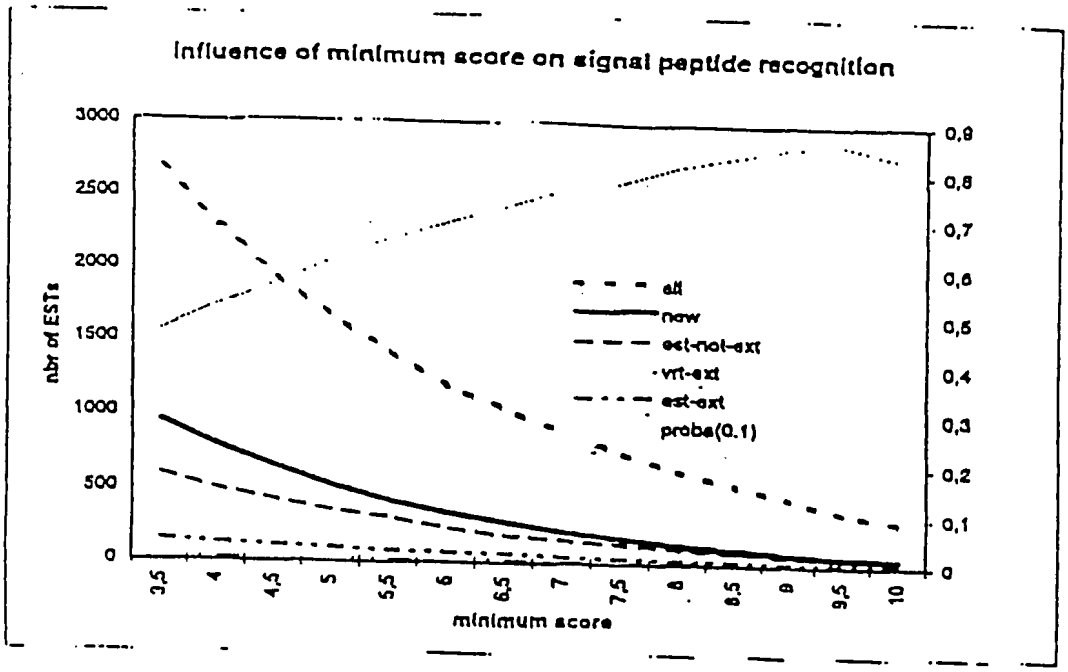


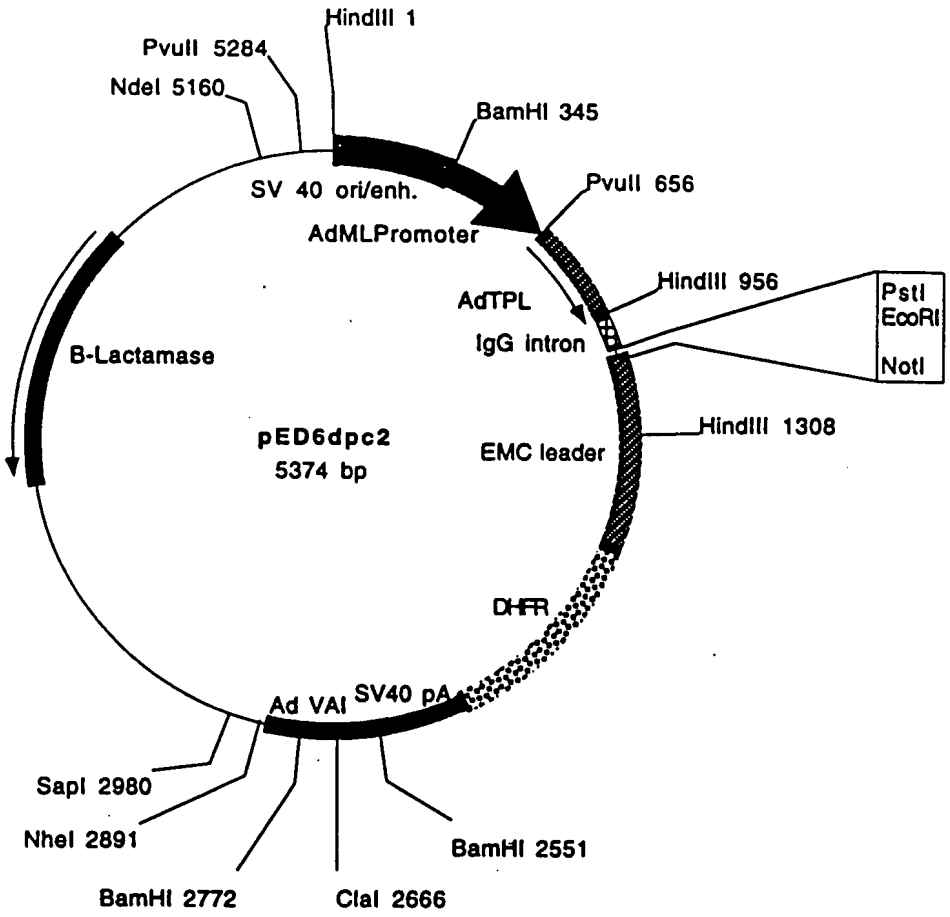
FIGURE 3

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3,5	2674	947	599	23	150
4	2278	784	488	23	126
4,5	1943	647	425	22	112
5	1657	523	353	21	96
5,5	1417	418	307	19	80
6	1180	340	238	18	68
6,5	1035	280	186	18	60
7	893	219	161	15	48
7,5	753	173	132	12	36
8	636	133	101	11	29
8,5	543	104	83	8	26
9	456	81	63	6	24
9,5	364	57	48	6	18
10	303	47	35	6	15

FIGURE 4

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	18	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart.	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	8	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	65	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

FIGURE 5



Plasmid name: pED6dpc2
Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 6

Description of Promoter structure isolated from SignalTag 5'ESTs

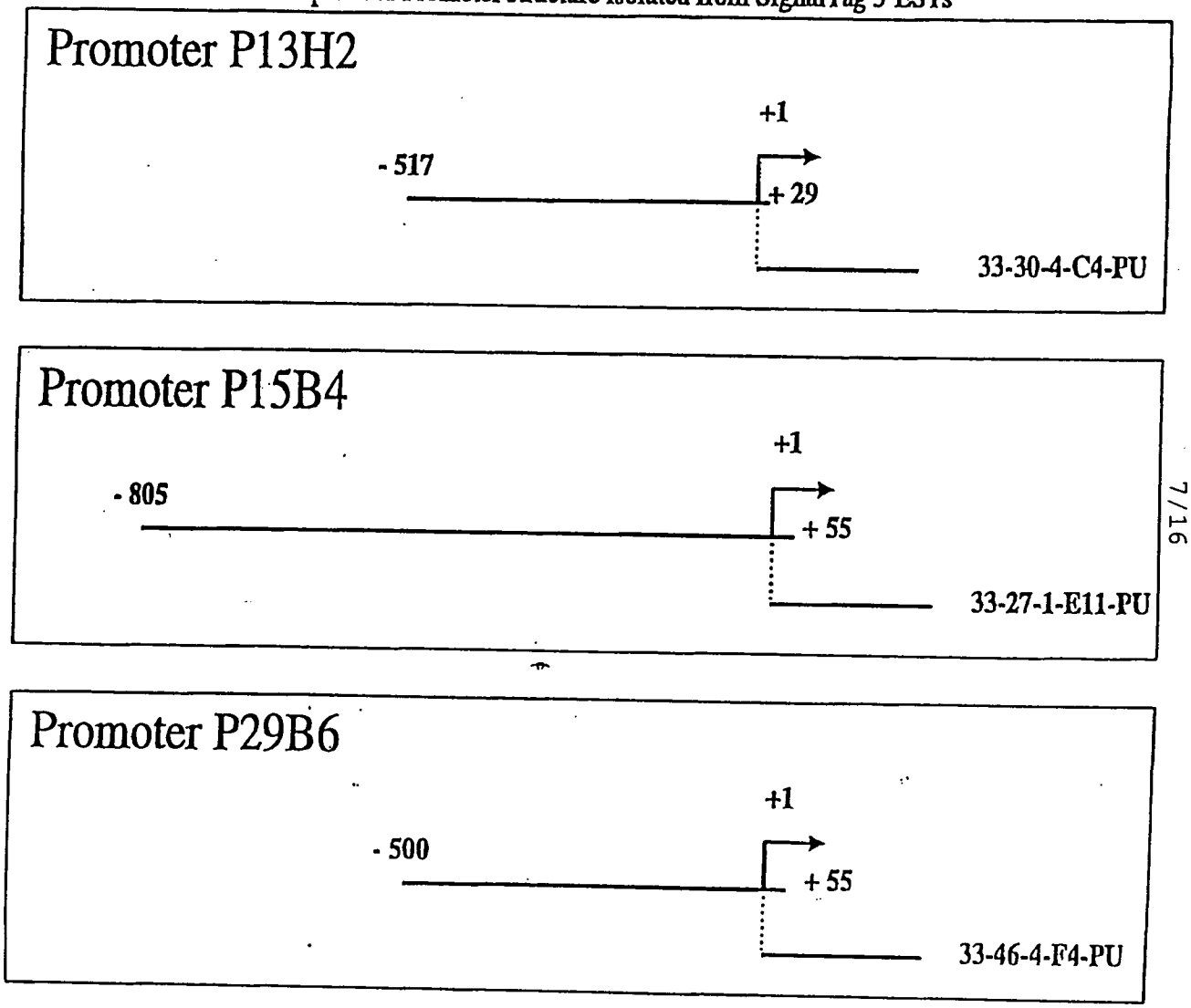


FIGURE 7

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences.

Promoter sequence P13H2 (548 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.963	9	TGTCAGTTG
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHAE47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETAE47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.960	14	TCAGTGATATGGCA
SRY_02	-41	-	0.961	12	TAAAACAAAACA
E2F_02	-33	+	0.957	8	TTTAGCGC
MZF1_01	-6	-	0.976	8	TGAGGGGA

Promoter sequence P1584 (661 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCCTGGAA
STAT_01	-673	-	0.951	9	TTCCAGGAA
MZF1_01	-656	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTTC
MZF1_01	-424	+	0.988	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

Promoter sequence P2966 (555 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.966	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT
CET81P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

Figure 8

98.2% identity in 113 aa overlap

```
                10        20        30        40        50        60
SeqID214 MVIRVYIASSSGSTAIKKKQQDVLGFLEANKIGFEEKDIAANEENRKWMRENVPENSRPA
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AF042081 MVIRVYIASSSGSTAIKKKQQDVLGFLEANKIGFEEKDIAANEENRKWMRENVPENSRPA
                10        20        30        40        50        60

                70        80        90       100       110
SeqID214 TGNPLPPQIFNESQYRGDYDAFFEARENNAVYAFLGLTAPSGSKEAEVQAKQQ
         :: ::::::::::::::::::::::::::::::::::::.:::::::::::::
AF042081 TGYPLPPQIFNESQYRGDYDAFFEARENNAVYAFLGLTAPPGSKEAEVQAKQQ
                70        80        90       100       110
```

FIGURE 9

```
seqID215    MADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVANDNAPEHALRPGFLSTFALATDQG
seqID185    MADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVVKVANDNAPEHALRPGFLSTFALATDQG
AF082526    MADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVANDSAPEHALRPGFLSTFALATDQG
            ********************************.***** *********************

seqID215    SKLGLSKNKSIICYYNTYQVVQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQV
seqID185    SKLGLSKNKSIICYYNTYQVVQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQV
AF082526    SKLGLSKNKSIICYYNTYQVVQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELIKV
            ********************************************************* .*

seqID215    VEVS
seqID185    VEVS
AF082526    VEVS
            ****
```

FIGURE 10

91.3% identity in 230 aa overlap

```
                10        20        30        40        50        60
SeqID186 MASLGLQLVGYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTG
         :::::.:::::::::::::::: .:::::.:.:::::::::::::::::::::::::::::
AF072128 MASLGVQLVGYILGLLGLLGTSIAMLLPNWRTSSYVGASIVTAVGFSKGLWMECATHSTG
                10        20        30        40        50        60

                70        80        90       100       110       120
SeqID186 ITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVA
         ::::::::::::::::::::::::::::::::.:::::::::::::::::::.:::::::::.
AF072128 ITQCDIYSTLLGLPADIQAAQAMMVTSSAMSSLACIISVVGMRCTVFCQDSRAKDRVAVV
                70        80        90       100       110       120

               130       140       150       160       170       180
SeqID186 GGVFFILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGII
         :::::::::.:::::::::::::::::::::::::::::::::::::::::.::::.::.:
AF072128 GGVFFILGGILGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISALFSLVAGVI
               130       140       150       160       170       180

               190       200       210       220       230
SeqID186 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
         :::::::.: ::.:::::.:::::::::::::..:.::.::::::::::::::
AF072128 LCFSCSPQGNRTNYYDGYQAQPLATRSSPRSAQQPKAKSEFNSYSLTGYV
               190       200       210       220       230
```

FIGURE 11

```
98.3% identity in 121 aa overlap

                                        10        20        30
seqID213                             RFRKETDNAAIIMKVDKDRQMVVLEEEFRNISPEELKME
                                     :::::::::::::::::::::::::::::.::::::::::
AB001993 MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
                  10        20        30        40        50        60

         40        50        60        70        80        90
seqID213 LPERQPRFVVYSYKYVRDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
         ::::::::::::::::::.:::::::::::::::::::::::::::::::::::::::::::
AB001993 LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                  70        80        90       100       110       120

       100       110       120
seqID213 FEIRTTDDLTEAWLQEKLSFFR
         ::::::::::::::::::::::
AB001993 FEIRTTDDLTEAWLQEKLSFFR
                  130       140
```

FIGURE 12

95.6% identity in 91 aa overlap

```
                                                          10        20
seq ID191                                                 MGCVFQSTEDKCIFKIDWTLS
                                                          :::::::::::::::::::::
W36955      MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
                    10        20        30        40        50        60

                   30        40        50        60        70        80
seq ID191   PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL
            :::::::::::::::::::::::::::::::: ::::::::::::...
W36955      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQDVE
                   70        80        90       100       110

                   90       100
seq ID191   KGESQVFKKAVVLHVLPEEPKGTQMLT
```

FIGURE 13

99.0% identity in 381 aa overlap;

```
                10        20        30        40        50        60
seqID200  MLLSIGMLMLSATQVYTVLTVQLFAFLNPLPVEADILAYNFENASQTFDDLPARFGYRLP
          :::::::::::::::::.:::::::::: :::::::::::::::::::::::::::::
AF037204  MLLSIGMLMLSATQVYTILTVQLFAFLNLLPVEADILAYNFENASQTFDDLPARFGYRLP
                10        20        30        40        50        60

                70        80        90       100       110       120
id200     AEGLKGFLINSKPENACEPIVPPPVKDNSSGTFIVLIRRLDCNFDIKVLNAQRAGYKAAI
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AF037204  AEGLKGFLINSKPENACEPIVPPPVKDNSSGTFIVLIRRLDCNFDIKVLNAQRAGYKAAI
                70        80        90       100       110       120

               130       140       150       160       170       180
id200     VHNVDSDDLISMGSNDIEVLKKIDIPSVFIGESSASSLKDEFTYEKGGHLILVPEFSLPL
          ::::::::::::::::::::::::::::::::::.:::::::::::::::::::::::::
AF037204  VHNVDSDDLISMGSNDIEVLKKIDIPSVFIGESSANSLKDEFTYEKGGHLILVPEFSLPL
               130       140       150       160       170       180

               190       200       210       220       230       240
id200     EYYLIPFLIIVGICLILIVIFMITKFVQDRHRARRNRLRKDQLKKLPVHKFKKGDEYDVC
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AF037204  EYYLIPFLIIVGICLILIVIFMITKFVQDRHRARRNRLRKDQLKKLPVHKFKKGDEYDVC
               190       200       210       220       230       240

               250       260       270       280       290       300
id200     AICLDEYEDGDKLRILPCSHAYHCKCVDPWLTKTKKTCPVCRQKVVPSQGDSDSDTDSSQ
          ::::::::::::::::::::::::::::::::::::::::::.::::::::::::::::::
AF037204  AICLDEYEDGDKLRILPCSHAYHCKCVDPWLTKTKKTCPVCKQKVVPSQGDSDSDTDSSQ
               250       260       270       280       290       300

               310       320       330       340       350       360
id200     EENEVTEHTPLLRPLASVSAQSFGALSESRSHQNMTESSDYEEDDNEDTDSSDAENEINE
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AF037204  EENEVTEHTPLLRPLASVSAQSFGALSESRSHQNMTESSDYEEDDNEDTDSSDAENEINE
               310       320       330       340       350       360

               370       380
id200     HDVVVQLQPNGERDYNIANTV
          :::::::::::::::::::::
AF037204  HDVVVQLQPNGERDYNIANTV
               370       380
```

FIGURE 14

```
100.0% identity in 68 aa overlap

                   10        20        30        40        50        60
seqID192   MSVFWGFVGFLVPWFIPKGPNRGVIITMLVTCSVCCYLFWLIAILAQLNPLFGPQLKNET
           ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Y15286     MSVFWGFVGFLVPWFIPKGPNRGVIITMLVTCSVCCYLFWLIAILAQLNPLFGPQLKNET
                 20        30        40        50        60        70

seqID192   IWYLKYHW
           ::::::::
Y15286     IWYLKYHW
                 80
```

FIGURE 15

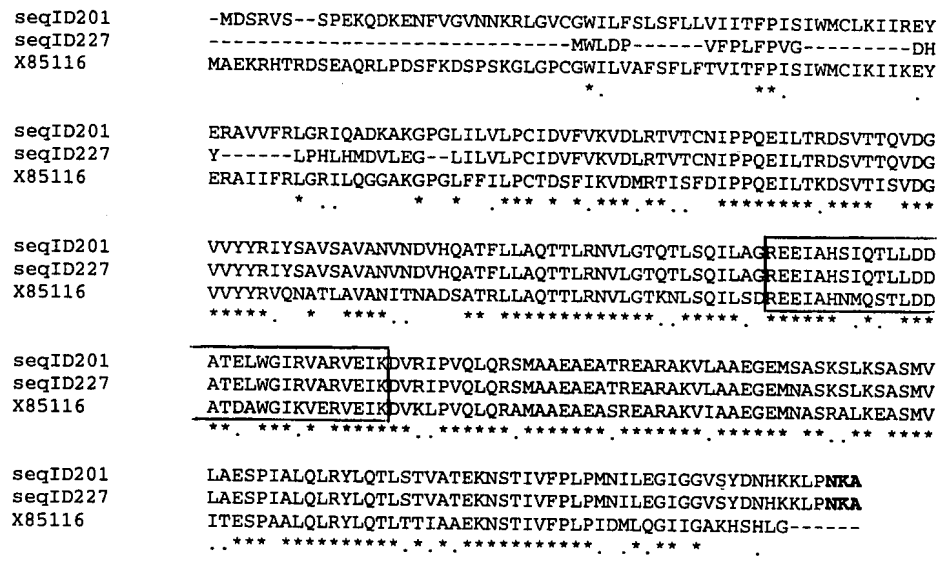

seqID201 -MDSRVS--SPEKQDKENFVGVNNKRLGVCGWILFSLSFLLVIITFPISIWMCLKIIREY
seqID227 ----------MWLDP------VFPLFPVG---------DH
X85116 MAEKRHTRDSEAQRLPDSFKDSPSKGLGPCGWILVAFSFLFTVITFPISIWMCIKIIKEY
seqID201 ERAVVFRLGRIQADKAKGPGLILVLPCIDVFVKVDLRTVTCNIPPQEILTRDSVTTQVDG
seqID227 Y------LPHLHMDVLEG--LILVLPCIDVFVKVDLRTVTCNIPPQEILTRDSVTTQVDG
X85116 ERAIIFRLGRILQGGAKGPGLFFILPCTDSFIKVDMRTISFDIPPQEILTKDSVTISVDG
seqID201 VVYYRIYSAVSAVANVNDVHQATFLLAQTTLRNVLGTQTLSQILAGREEIAHSIQTLLDD
seqID227 VVYYRIYSAVSAVANVNDVHQATFLLAQTTLRNVLGTQTLSQILAGREEIAHSIQTLLDD
X85116 VVYYRVQNATLAVANITNADSATRLLAQTTLRNVLGTKNLSQILSDREEIAHNMQSTLDD
seqID201 ATELWGIRVARVEIKDVRIPVQLQRSMAAEAEATREARAKVLAAEGEMSASKSLKSASMV
seqID227 ATELWGIRVARVEIKDVRIPVQLQRSMAAEAEATREARAKVLAAEGEMNASKSLKSASMV
X85116 ATDAWGIKVERVEIKDVKLPVQLQRAMAAEAEASREARAKVIAAEGEMNASRALKEASMV
seqID201 LAESPIALQLRYLQTLSTVATEKNSTIVFPLPMNILEGIGGVSYDNHKKLPNKA
seqID227 LAESPIALQLRYLQTLSTVATEKNSTIVFPLPMNILEGIGGVSYDNHKKLPNKA
X85116 ITESPAALQLRYLQTLTTIAAEKNSTIVFPLPIDMLQGIIGAKHSHLG------

FIGURE 16